

p779.ST25
SEQUENCE LISTING

<110> Porro, Danilo

<120> Process for expression and secretion of proteins by the non-conventional yeast *Zygosaccharomyces bailii*

<130> p 779wo

<150> DE 10252245.6

<151> 2003-11-07

<160> 95

<170> PatentIn version 3.1

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35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
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35 40 45

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50 55 60

Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
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Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
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gagcttgacg gggaaagccg gcgaacgtgg cgagaaagga agggaagaaa gcgaaaggag	120
cgggcgctag ggcgctggca agtgtagcgg tcacgctgcg cgtaaccacc acaccgccc	180
cgcttaatgc gccgctacag ggcgcgtcag gtggcacttt tcgggggaaat gtgcgcggaa	240
cccctatttg ttattttttc taaatacatt caaatatgta tccgctcatg agacaataa	299

<210> 66

<211> 153

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 66

ctccactgta acatttccca ctgtcctttt cccatctttc attttacaat gagcaagttt	60
cagaaaaaaa aatacaaatg ggataagtgc aaaacattcc atgtatctgt agcttccaat	120
gttattcctc tctccagagt caggcttctg tgt	153

<210> 67

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<211> 231

<212> DNA

<213> Zygosaccharomyces bailii

<400> 67

aattcaatag atgatgattt aacttcattt aatgagaaga tttcattaga ttcaacaaaa	60
tctggagatt ttgcataaac aactgattta ttattagctt tattttctaa tccattaact	120
aattgatcat acataatata gatgaataag aataatgaaa ctagtgcaat aattgatcca	180
attgatgcta cataatttca accagcaaag gcatcagggt agtcaggaat t	231

<210> 68

<211> 52

<212> DNA

<213> Zygosaccharomyces bailii

<400> 68

ctcgtaaaaa cgagcatgag ctgctgcagg tcagccgtgg atatcgttgc gg	52
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<210> 69

<211> 116

<212> DNA

<213> Zygosaccharomyces bailii

<400> 69

ctatctgcac gtgccaccgg aggtgctgtg ggagcgactg cggcacgata gccatcggcc	60
gctgctgcag gtgccgcagc cgaggcagcg cattttcgaa ctctacgccc agcgcg	116

<210> 70

<211> 268

<212> DNA

<213> Zygosaccharomyces bailii

<400> 70

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cctgggcata attgagcaaa tcgtactcgt gcgcggcgat gcgctccttg ccgatcgaat	120
tgacgtaatc gatcgcgggc cgcagcccga tcgcctcgac gatcggcggc gtgccggcct	180
cgaacttgat cggcggggtc ccataggtga cccagtcctt ggcaacttca cggatcattt	240
cgccgcccgc gttgaacggc cgcacgac	268

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<210> 71
<211> 869
<212> DNA
<213> Zygosaccharomyces bailii

<400> 71
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tcggtaccac gcatgctgca gacgcgttac gtatcggatc cagaattcgt gatattctat 120
tgggtatgtc ccctgattcg acggcgtaaa ttgctggaat cttgtgttgg cgctaatac 180
cgcttttttg aattatgtgc tatgcctctg ccattgggtat caacagctga aatatttggt 240
gaagatcgaa tatcttctat tgtttctgag ggtatccccg aagctatggc gaaagaaagg 300
atctcttctc gtacttggat cggtagcaga agcaatagac gcacaatgca ttgacgcac 360
ttgttgatac cgggtaaatgt gagtcttctg gggtctgtta ttgagtttaa tatgtcgtcc 420
acctctgttc tcgtatccat ttgtagagta gcccgccata cagcacgtcc aatacaggag 480
aggccattta gcttcagggtg cagagaagac acagcatggg gctcaccttc gagtgtctca 540
atagatgatt gagttgactg ggcttccgtg aaagggcctt tcgagagatc ttcagaaata 600
aaccagggtt gcgcttcatt agtaggtgtt cctggaggac tattgtcgct atctgctgga 660
ctactgctac caagtagtga aggggggtatt ctaaggcttt cactctgttc tgacactatt 720
ataacattgc caaggccaat ttgaaagggt tcgctgtatat gagtaaagag ctcggtgccc 780
ttccagttgg aatcaagccg ttcaagcaga tcgagagcat aatcagagtc cacatttccg 840
cacgcaagag agaactctga gttcattct 869

<210> 72
<211> 1425
<212> DNA
<213> Zygosaccharomyces bailii

<220>
<221> CDS
<222> (1) .. (1425)
<223>

<400> 72
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1 5 10 15

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gca	gaa	ata	aag	cgt	att	ttg	agt	cgc	ggc	gac	cct	ata	cct	tta	caa	96
Ala	Glu	Ile	Lys	Arg	Ile	Leu	Ser	Arg	Gly	Asp	Pro	Ile	Pro	Leu	Gln	
			20					25					30			
agg	tta	gct	tct	cta	cta	act	atg	gtg	atc	cta	acg	gtc	aac	atg	tca	144
Arg	Leu	Ala	Ser	Leu	Leu	Thr	Met	Val	Ile	Leu	Thr	Val	Asn	Met	Ser	
		35					40					45				
aaa	aag	agg	aag	agc	tct	cca	atc	aag	ctt	agc	acc	ttt	act	aaa	tat	192
Lys	Lys	Arg	Lys	Ser	Ser	Pro	Ile	Lys	Leu	Ser	Thr	Phe	Thr	Lys	Tyr	
	50					55					60					
cgt	aga	aat	gtt	gcg	aag	tca	ttg	tat	tat	gat	atg	tca	agc	aag	aca	240
Arg	Arg	Asn	Val	Ala	Lys	Ser	Leu	Tyr	Tyr	Asp	Met	Ser	Ser	Lys	Thr	
65					70					75					80	
gta	ttc	ttc	gaa	tac	cat	ctc	aaa	aat	aca	caa	gat	cta	cag	gag	ggc	288
Val	Phe	Phe	Glu	Tyr	His	Leu	Lys	Asn	Thr	Gln	Asp	Leu	Gln	Glu	Gly	
				85					90					95		
ctc	gag	caa	gcc	att	gcg	ccc	tac	aat	ttc	gtg	gta	aag	gtg	cac	aag	336
Leu	Glu	Gln	Ala	Ile	Ala	Pro	Tyr	Asn	Phe	Val	Val	Lys	Val	His	Lys	
			100					105					110			
aag	cca	att	gat	tgg	cag	aaa	cag	ctc	tca	agc	gtg	cat	gag	agg	aaa	384
Lys	Pro	Ile	Asp	Trp	Gln	Lys	Gln	Leu	Ser	Ser	Val	His	Glu	Arg	Lys	
		115					120					125				
gcg	ggc	cac	aga	agc	att	ctc	agc	aac	aat	gtt	ggc	gcc	gag	atc	tct	432
Ala	Gly	His	Arg	Ser	Ile	Leu	Ser	Asn	Asn	Val	Gly	Ala	Glu	Ile	Ser	
	130					135					140					
aaa	ctg	gct	gag	acg	aaa	gat	tct	act	tgg	agt	ttt	atc	gag	aga	aca	480
Lys	Leu	Ala	Glu	Thr	Lys	Asp	Ser	Thr	Trp	Ser	Phe	Ile	Glu	Arg	Thr	
145					150					155					160	
atg	gat	ctg	ata	gaa	gcc	cgc	acc	cgc	cag	ccc	acg	aca	aga	gtt	gcg	528
Met	Asp	Leu	Ile	Glu	Ala	Arg	Thr	Arg	Gln	Pro	Thr	Thr	Arg	Val	Ala	
				165					170					175		
tat	agg	ttt	ctg	ctt	caa	ctc	aca	ttc	atg	aac	tgc	tgt	agg	gct	aat	576
Tyr	Arg	Phe	Leu	Leu	Gln	Leu	Thr	Phe	Met	Asn	Cys	Cys	Arg	Ala	Asn	
			180					185					190			
gat	ttg	aaa	aac	gcc	gac	ccc	agc	act	ttt	caa	atc	atc	gca	gat	cct	624
Asp	Leu	Lys	Asn	Ala	Asp	Pro	Ser	Thr	Phe	Gln	Ile	Ile	Ala	Asp	Pro	
		195				200						205				
cac	ctt	ggt	cgt	ata	ttg	cgg	gcc	ttt	gtt	cca	gag	aca	aag	act	agc	672
His	Leu	Gly	Arg	Ile	Leu	Arg	Ala	Phe	Val	Pro	Glu	Thr	Lys	Thr	Ser	
	210					215					220					
att	gaa	agg	ttt	atc	tat	ttt	ttc	cca	tgt	aag	gga	cga	tgc	gat	ccg	720
Ile	Glu	Arg	Phe	Ile	Tyr	Phe	Phe	Pro	Cys	Lys	Gly	Arg	Cys	Asp	Pro	
225					230					235					240	
ctt	ttg	gct	cta	gat	tcc	tat	ctc	ctg	tgg	gtt	ggc	cca	gtg	ccc	aaa	768
Leu	Leu	Ala	Leu	Asp	Ser	Tyr	Leu	Leu	Trp	Val	Gly	Pro	Val	Pro	Lys	
				245					250					255		
act	cag	act	acc	gat	gaa	gag	act	caa	tat	gat	tac	cag	ctt	ctt	caa	816
Thr	Gln	Thr	Thr	Asp	Glu	Glu	Thr	Gln	Tyr	Asp	Tyr	Gln	Leu	Leu	Gln	
			260					265					270			
gat	act	ctc	ttg	att	tcg	tac	gac	agg	ttt	atc	gcc	aaa	gaa	tca	aag	864
Asp	Thr	Leu	Leu	Ile	Ser	Tyr	Asp	Arg	Phe	Ile	Ala	Lys	Glu	Ser	Lys	
		275					280					285				

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gaa Glu	aat Asn 290	att Ile	ttc Phe	aaa Lys	ata Ile	cct Pro 295	aat Asn	ggg Gly	ccc Pro	aaa Lys	gct Ala 300	cat His	ttg Leu	ggg Gly	cgg Arg	912
cat His 305	cta Leu	atg Met	gca Ala	tca Ser	tac Tyr 310	ctt Leu	gga Gly	aac Asn	aac Asn	agt Ser 315	ctc Leu	aag Lys	agc Ser	gag Glu	gcc Ala 320	960
aca Thr	ctc Leu	tac Tyr	ggc Gly	aac Asn 325	tgg Trp	tct Ser	gtg Val	gaa Glu	agg Arg 330	caa Gln	gag Glu	ggc Gly	gtc Val	agc Ser 335	aaa Lys	1008
atg Met	gct Ala	gac Asp	agc Ser 340	cga Arg	tac Tyr	atg Met	cac His	acg Thr 345	gtt Val	aaa Lys	aaa Lys	agt Ser	cca Pro 350	cct Pro	tca Ser	1056
tat Tyr	cta Leu	ttt Phe 355	gca Ala	ttt Phe	tta Leu	tcc Ser	ggc Gly 360	tac Tyr	tac Tyr	aaa Lys	aag Lys	tcc Ser 365	aac Asn	caa Gln	ggc Gly	1104
gag Glu	tac Tyr 370	gtg Val	ctg Leu	gct Ala	gaa Glu	aca Thr 375	ctg Leu	tat Tyr	aat Asn	ccc Pro	ctg Leu 380	gat Asp	tac Tyr	gac Asp	aaa Lys	1152
aca Thr 385	ctt Leu	cca Pro	ata Ile	aca Thr	acg Thr 390	aac Asn	gag Glu	aaa Lys	ttg Leu	atc Ile 395	tgt Cys	cgg Arg	cgg Arg	tac Tyr	ggg Gly 400	1200
aaa Lys	aat Asn	gcg Ala	aaa Lys	gtg Val 405	ata Ile	cca Pro	aaa Lys	gac Asp	gca Ala 410	ctg Leu	ctg Leu	tat Tyr	ctc Leu	tac Tyr 415	acg Thr	1248
tat Tyr	gcg Ala	cag Gln	cag Gln 420	aag Lys	cga Arg	aaa Lys	caa Gln	ttg Leu 425	gcc Ala	gat Asp	ccc Pro	aat Asn	gag Glu 430	caa Gln	aat Asn	1296
agg Arg	cta Leu	ttc Phe 435	agt Ser	agt Ser	gaa Glu	tca Ser	cca Pro 440	gcg Ala	cat His	ccc Pro	ttc Phe	tta Leu 445	act Thr	cct Pro	caa Gln	1344
tcg Ser	aca Thr 450	ggc Gly	tca Ser	tcg Ser	aca Thr	ccc Pro 455	ttg Leu	acc Thr	tgg Trp	act Thr	gct Ala 460	cca Pro	aag Lys	aca Thr	ctc Leu	1392
tcc Ser 465	act Thr	ggt Gly	cta Leu	atg Met	aca Thr 470	cct Pro	gga Gly	gaa Glu	gag Glu	tag						1425

<210> 73

<211> 474

<212> PRT

<213> Zygosaccharomyces bailii

<400> 73

Met 1	Ser	Glu	Phe	Ser 5	Glu	Leu	Val	Arg	Ile 10	Leu	Pro	Leu	Asp	Gln	Val 15
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Ala	Glu	Ile	Lys 20	Arg	Ile	Leu	Ser	Arg 25	Gly	Asp	Pro	Ile	Pro 30	Leu	Gln
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

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Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser
35 40 45

Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr
50 55 60

Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr
65 70 75 80

Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly
85 90 95

Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys
100 105 110

Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys
115 120 125

Ala Gly His Arg Ser Ile Leu Ser Asn Asn Val Gly Ala Glu Ile Ser
130 135 140

Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr
145 150 155 160

Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala
165 170 175

Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn
180 185 190

Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro
195 200 205

His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser
210 215 220

Ile Glu Arg Phe Ile Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro
225 230 235 240

Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys
245 250 255

Thr Gln Thr Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln
260 265 270

Asp Thr Leu Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys
275 280 285

Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg
290 295 300

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His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala
 305 310 315 320
 Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys
 325 330 335
 Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser
 340 345 350
 Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly
 355 360 365
 Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys
 370 375 380
 Thr Leu Pro Ile Thr Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly
 385 390 395 400
 Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr
 405 410 415
 Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn
 420 425 430
 Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln
 435 440 445
 Ser Thr Gly Ser Ser Thr Pro Leu Thr Trp Thr Ala Pro Lys Thr Leu
 450 455 460
 Ser Thr Gly Leu Met Thr Pro Gly Glu Glu
 465 470

<210> 74

<211> 1074

<212> DNA

<213> Zygosaccharomyces bailii

<220>

<221> CDS

<222> (1)..(1074)

<223>

<400> 74

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48

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aag Lys	atg Met	atc Ile	ttt Phe 20	gat Asp	gtg Val	ctt Leu	atg Met	aca Thr 25	ttt Phe	cct Pro	tac Tyr	ttc Phe	gcg Ala 30	gta Val	cat His
ggt Val	cct Pro	tcc Ser 35	aag Lys	aat Asn	ata Ile	ctt Leu	atc Ile 40	aca Thr	cca Pro	aaa Lys	ggc Gly	aca Thr 45	ggt Val	gag Glu	ata Ile
cct Pro	gaa Glu 50	aac Asn	tat Tyr	caa Gln	aat Asn	tat Tyr 55	ccc Pro	ata Ile	ttg Leu	gcc Ala	atc Ile 60	ttc Phe	tac Tyr	gtc Val	aaa Lys
tat Tyr 65	tta Leu	atg Met	aag Lys	aaa Lys	aat Asn 70	ccg Pro	tac Tyr	gat Asp	ctt Leu	ctt Leu 75	cca Pro	agc Ser	acc Thr	gtg Val	aac Asn 80
tgg Trp	ccg Pro	gaa Glu	ccc Pro	tat Tyr 85	gta Val	gtg Val	gtg Val	aat Asn	acc Thr 90	atc Ile	act Thr	aag Lys	cgt Arg	ttc Phe 95	cag Gln
gac Asp	cat His	aaa Lys	cta Leu 100	ttt Phe	gca Ala	aac Asn	aaa Lys	aat Asn 105	gct Ala	gat Asp	gtc Val	tac Tyr	ggt Val 110	gaa Glu	aga Arg
ctt Leu	caa Gln	aat Asn 115	gca Ala	att Ile	gcc Ala	tcg Ser	ggt Gly 120	att Ile	aag Lys	att Ile	cct Pro	gag Glu 125	tct Ser	aag Lys	aag Lys
aat Asn 130	gaa Glu	cga Arg	tta Leu	ggg Gly	cag Gln	cca Pro 135	aaa Lys	aag Lys	acg Thr	aaa Lys	aat Asn 140	ggt Val	aca Thr	aaa Lys	gag Glu
att Ile 145	gag Glu	gag Glu	acc Thr	ttt Phe	att Ile 150	gat Asp	gcc Ala	act Thr	aat Asn	gcg Ala 155	aga Arg	aaa Lys	gaa Glu	ttg Leu	gat Asp 160
gag Glu	tac Tyr	ttc Phe	aga Arg	aaa Lys 165	ctt Leu	cag Gln	gat Asp	ggt Gly	aca Thr 170	tta Leu	acc Thr	gga Gly	gat Asp	ttg Leu 175	gag Glu
ggt Gly	ggc Gly	ttg Leu	tgc Cys 180	aag Lys	gtc Val	aaa Lys	acg Thr	ctc Leu 185	ata Ile	tcg Ser	tgt Cys	aaa Lys	gct Ala 190	ttg Leu	ttc Phe
gga Gly	gga Gly	cac His 195	acc Thr	caa Gln	gaa Glu	ctc Leu	cag Gln 200	ttt Phe	atg Met	gcc Ala	acc Thr	aat Asn 205	ggt Val	cgt Arg	aaa Lys
gtc Val	tgg Trp 210	ata Ile	ggg Gly	gag Glu	ata Ile	gtg Val 215	tgc Cys	ggc Gly	atg Met	ggt Val	tcc Ser 220	aat Asn	aaa Lys	aat Asn	gca Ala
att Ile 225	gac Asp	gat Asp	aat Asn	gat Asp	ctc Leu 230	gag Glu	gaa Glu	gaa Glu	gag Glu	cgt Arg 235	aat Asn	gca Ala	tcg Ser	ggc Gly	gaa Glu 240
caa Gln	act Thr	acg Thr	aca Thr	gcc Ala 245	cga Arg	gag Glu	gaa Glu	tca Ser	gag Glu 250	gct Ala	ctg Leu	gat Asp	acc Thr	aca Thr 255	tcc Ser
aat Asn	ggt Gly	ttg Leu	gac Asp 260	gct Ala	ctg Leu	aat Asn	act Thr	caa Gln 265	att Ile	aat Asn	gcc Ala	ata Ile	gaa Glu 270	acg Thr	gag Glu
gaa	tca	ttt	tgg	gaa	gct	atc	agg	gcg	ctc	cat	aat	gag	cta	cgc	acc

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Glu	Ser	Phe	Trp	Glu	Ala	Ile	Arg	Ala	Leu	His	Asn	Glu	Leu	Arg	Thr		
		275					280					285					
tct	cca	aca	cag	tta	gaa	gag	tgc	agg	aaa	gcg	gca	gtt	ttt	tta	ctg		912
Ser	Pro	Thr	Gln	Leu	Glu	Glu	Cys	Arg	Lys	Ala	Ala	Val	Phe	Leu	Leu		
		290				295					300						
ggc	cat	aaa	aaa	ata	ctc	caa	aca	ttt	aca	aag	caa	aag	gat	act	gcc		960
Gly	His	Lys	Lys	Ile	Leu	Gln	Thr	Phe	Thr	Lys	Gln	Lys	Asp	Thr	Ala		
					310					315					320		
cgc	gct	ctt	ttt	tat	ata	aat	ctc	aaa	gag	tgt	ctg	gga	acc	agc	tgg		1008
Arg	Ala	Leu	Phe	Tyr	Ile	Asn	Leu	Lys	Glu	Cys	Leu	Gly	Thr	Ser	Trp		
				325					330					335			
aat	tta	gaa	tat	aca	gag	gca	tca	gat	gca	aga	aaa	atg	gca	att	aaa		1056
Asn	Leu	Glu	Tyr	Thr	Glu	Ala	Ser	Asp	Ala	Arg	Lys	Met	Ala	Ile	Lys		
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Gly	Glu	Leu	Gln	Asn													
		355															

<210> 75

<211> 357

<212> PRT

<213> Zygosaccharomyces bailii

<400> 75

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Lys	Met	Ile	Phe	Asp	Val	Leu	Met	Thr	Phe	Pro	Tyr	Phe	Ala	Val	His
			20					25					30		

Val	Pro	Ser	Lys	Asn	Ile	Leu	Ile	Thr	Pro	Lys	Gly	Thr	Val	Glu	Ile
		35					40					45			

Pro	Glu	Asn	Tyr	Gln	Asn	Tyr	Pro	Ile	Leu	Ala	Ile	Phe	Tyr	Val	Lys
	50					55					60				

Tyr	Leu	Met	Lys	Lys	Asn	Pro	Tyr	Asp	Leu	Leu	Pro	Ser	Thr	Val	Asn
65					70					75					80

Trp	Pro	Glu	Pro	Tyr	Val	Val	Val	Asn	Thr	Ile	Thr	Lys	Arg	Phe	Gln
				85					90					95	

Asp	His	Lys	Leu	Phe	Ala	Asn	Lys	Asn	Ala	Asp	Val	Tyr	Val	Glu	Arg
			100					105					110		

Leu	Gln	Asn	Ala	Ile	Ala	Ser	Gly	Ile	Lys	Ile	Pro	Glu	Ser	Lys	Lys
		115					120					125			

p779.ST25
Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu
130 135 140
Ile Glu Glu Thr Phe Ile Asp Ala Thr Asn Ala Arg Lys Glu Leu Asp
145 150 155 160
Glu Tyr Phe Arg Lys Leu Gln Asp Gly Thr Leu Thr Gly Asp Leu Glu
165 170 175
Gly Gly Leu Cys Lys Val Lys Thr Leu Ile Ser Cys Lys Ala Leu Phe
180 185 190
Gly Gly His Thr Gln Glu Leu Gln Phe Met Ala Thr Asn Val Arg Lys
195 200 205
Val Trp Ile Gly Glu Ile Val Cys Gly Met Val Ser Asn Lys Asn Ala
210 215 220
Ile Asp Asp Asn Asp Leu Glu Glu Glu Glu Arg Asn Ala Ser Gly Glu
225 230 235 240
Gln Thr Thr Thr Ala Arg Glu Glu Ser Glu Ala Leu Asp Thr Thr Ser
245 250 255
Asn Gly Leu Asp Ala Leu Asn Thr Gln Ile Asn Ala Ile Glu Thr Glu
260 265 270
Glu Ser Phe Trp Glu Ala Ile Arg Ala Leu His Asn Glu Leu Arg Thr
275 280 285
Ser Pro Thr Gln Leu Glu Glu Cys Arg Lys Ala Ala Val Phe Leu Leu
290 295 300
Gly His Lys Lys Ile Leu Gln Thr Phe Thr Lys Gln Lys Asp Thr Ala
305 310 315 320
Arg Ala Leu Phe Tyr Ile Asn Leu Lys Glu Cys Leu Gly Thr Ser Trp
325 330 335
Asn Leu Glu Tyr Thr Glu Ala Ser Asp Ala Arg Lys Met Ala Ile Lys
340 345 350
Gly Glu Leu Gln Asn
355

<210> 76

<211> 750

<212> DNA

<213> Zygosaccharomyces bailii

p779.ST25

<220>

<221> CDS

<222> (1)..(750)

<223>

<400> 76

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gct ctc gat ctg ctt gaa cgg ctt gat tcc aac tgg aag ggc acc gag	96
Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu	
20 25 30	
ctc ttt act cat ata cgc gaa acc ttt caa att ggc ctt ggc aat gtt	144
Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val	
35 40 45	
atc ata gtg tca gaa cag agt gaa agc ctt aga ata ccc cct tca cta	192
Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu	
50 55 60	
ctt ggt agc agt agt cca gca gat agc gac aat agt cct cca gga aca	240
Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr	
65 70 75 80	
cct act aat gaa gcg caa ccc tgg ttt att tct gaa gat ctc tcg aaa	288
Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys	
85 90 95	
ggc cct ttc acg gaa gcc cag tca act caa tca tct att gag aca ctc	336
Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu	
100 105 110	
gaa ggt gag cac cat gct gtg tct tct ctg cac ctg aag cta aat ggc	384
Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly	
115 120 125	
ctc tcc tgt att gga cgt gct gta tgg cgg gct act cgc aaa atg gat	432
Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp	
130 135 140	
acg aga aca gag gtg gac gac ata tta aac tca ata aca gaa ccc aga	480
Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg	
145 150 155 160	
aga ctc aca tta ccc ggt atc aac aag atg cgt caa tgc att gtg cgt	528
Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg	
165 170 175	
cta ttg ctt ctc gta ccg atc caa gta cga gaa gag atc ctt tct ttc	576
Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe	
180 185 190	
gcc ata gct tcg ggg ata ccc tca gaa aca ata gaa gat att cga tct	624
Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser	
195 200 205	
tca aca aat att tca gct gtt gat acc aat ggc aga ggc ata gca cat	672
Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His	
210 215 220	

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aat tcc aaa aag cgg tca tta gcg cca aca caa gat tca cgc aat tta 720
 Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
 225 230 235 240

cgc cgt cga atc agg gga cat acc caa tag 750
 Arg Arg Arg Ile Arg Gly His Thr Gln
 245

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<211> 249

<212> PRT

<213> Zygosaccharomyces bailii

<400> 77

Met Asn Ser Glu Phe Ser Leu Ala Tyr Gly Asn Val Asp Ser Asp Tyr
 1 5 10 15

Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu
 20 25 30

Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val
 35 40 45

Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu
 50 55 60

Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr
 65 70 75 80

Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys
 85 90 95

Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu
 100 105 110

Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly
 115 120 125

Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp
 130 135 140

Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg
 145 150 155 160

Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg
 165 170 175

Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe
 180 185 190

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Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser
195 200 205

Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His
210 215 220

Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
225 230 235 240

Arg Arg Arg Ile Arg Gly His Thr Gln
245

<210> 78

<211> 453

<212> DNA

<213> *Saccharomyces cerevisiae*

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<223>

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<222> (451)..(453)

<223> start codon

<400> 78
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agtttttaat cttcagtggc atgtgagatt ctccgaaatt aattaaagca atcacacaat 180
tctctcggat accacctcgg ttgaaactga caggtgggtt gttacgcatg ctaatgcaaa 240
ggagcctata tacctttggc tcggctgctg taacagggaa tataaagggc agcataattt 300
aggagtttag tgaacttgca acatttacta ttttcccttc ttacgtaaata atttttcttt 360
ttaattctaa atcaatcttt ttcaattttt tgtttgatatt cttttcttgc ttaaattctat 420
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<210> 79

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<211> 499

<212> DNA

<213> *Zyg saccharomyces bailii*

<220>

<221> promoter

<222> (1)..(496)

<223>

<220>

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<222> (497)..(499)

<223> start codon

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cgtgtatcca ttgatactg tgctgggttac aagacacatg ctttacaagc acacttctat 180
ctctctcgac tgaggcgaaa cgtcgagtgg ttgatatca aatgcatgcg tgatatgcac 240
cattatTTTT cccttttact tccgtcacgc cggggctcca cttttttggg ttccactttt 300
cttacgaccc tcgacatcca ctaaacgaac aggaagtcaa agaaccctc gagtcacacg 360
gtgcgtatgc gctgttaaca tatataaagg tcacctttcc ctgctcaaaa gagtccttagc 420
aggctgttaa cttcactctc tatcgatcca tagaatctaa ctaacaagag actacatcgg 480
tataacaaat aacaaaatg 499

<210> 80

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 80
aagagactcc aacgtcgcg acctgta

27

<210> 81

p779.ST25

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 81

agaggattag gaagacacaa attgcatggt ga

32

<210> 82

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 82

atcgtattgc ttccattctt cttttgtta

29

<210> 83

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 83

tttgttattt gttataccga tgtagtctc

29

<210> 84

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 84

tagctactct tctccagggtg tcattag

27

p779.ST25

<210> 85

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 85

cctatgtccg agtttagcga gcttg

25

<210> 86

<211> 25

<212> DNA

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<220>

<223> PCR primer

<400> 86

agaatgaact cagagttctc tcttg

25

<210> 87

<211> 22

<212> DNA

<213> artificial sequence

<220>

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attctattgg gtatgtcccc tg

22

<210> 88

<211> 30

<212> DNA

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<220>

p779.ST25

<223> PCR primer

<400> 88
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30

<210> 89

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 89
attatgttct ccagggaaga ggtag

26

<210> 90

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 90
agaatcaatc atttagtgtg gcaggag

27

<210> 91

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 91
taaaaactgc ccgcatatt tcgtc

25

<210> 92

<211> 708

<212> DNA

<213> Zygosaccharomyces rouxi

p779.ST25

<400> 92
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tcctctcccc ctcccctttt tttccttctt tctttccatc tattttctgat ctctctcccct 180
cagcagatgt cccgaaaggt acagctgcga tacgggcagc cactttttga cgtctcgcaa 240
caggatcacc ctgcacgacg gggcacaata ggattcccgt tggcacgggtg ctgggtgtata 300
gccgccgagg gtgggggtata aagggtctaca tccttaccctt cacgcaggcg ataaccgca 360
tcatacaact gtcctcctct tccgctctcg ccactagccg ccgaaccatt gctaccgcaa 420
tgacaccgtg tggatgatctc aaggaggat gtgtgggtgt gggacggaac ttccactttt 480
tcctcagtag gtgcgatgcc ccctacaccg agcttccact aacgtgtttc agcggttgaa 540
ggcaatggga tcgcagaatt atcgcagctt gttggtatat aaaggagaa gatatatgga 600
taagagacat gttctacttc tgttctctct ttctttttat cctatatcac cagaacaaat 660
caagttcgca ttgattcata tcaaataaaa agtacatcac agataaca 708

<210> 93

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 93

TGCAGAAAGC CCTAAGATGC T

21

<210> 94

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 94

TGTCTGTGAT GTACTTTTTA TTTGATATG

29

<210> 95

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 95

ACGCAAGAGA GAACTCTGAG TTCAT

25